

Expanding genomics of mycorrhizal symbiosis

frontiers in
MICROBIOLOGY

MINI REVIEW ARTICLE

published: 04 November 2014

doi: 10.3389/fmicb.2014.00682



Expanding genomics of mycorrhizal symbiosis

Alan Kuo¹, Annegret Kohler², Francis M. Martin^{2*} and Igor V. Grigoriev^{1*}

¹ *United States Department of Energy Joint Genome Institute, Walnut Creek, CA, USA*

² *UMR, Lab of Excellence for Advanced Research on the Biology of Tree and Forest Ecosystems, Tree-Microbe Interactions, Institut National de la Recherche Agronomique, Université de Lorraine, Nancy, France*

Valeria Flores Almaraz
31 de octubre de 2018

Simbiosis micorrízica

- Mutualismo **ubícuo**.
- Juega un papel importante en la nutrición de la planta, “soil health” y en el ciclo del carbono.
- La simbiosis evolucionó **repetidamente** e **independientemente** en múltiples clados fúngicos.

Ancient

Among early land plants 410 ma

Pervasive

Underpins most terrestrial ecosystem,
the soil portion of the global carbon budget,
and much agricultural production

Las micorrizas pueden proveer de tolerancia al estrés y desintoxicación metálica a la planta hospedera

The fundamental transnacional logic of the symbiosis is the exchange of sugar photosynthesized by the plant for phosphorus and other nutrient acquired by the fungus.

Un objetivo principal en los estudios sobre micorrizas es definir la simbiosis en términos moleculares. Identificar los “genes de la simbiosis”.



Aquellos que codifican las moléculas que medían y regulan el desarrollo de la simbiosis y vías metabólicas interespecíficas

La diversidad de las micorrizas proporciona la oportunidad de una variedad igualmente diversa de métodos de investigación.

Un gran número de estudios fisiológicos, ecológicos y moleculares han sido desarrollados.

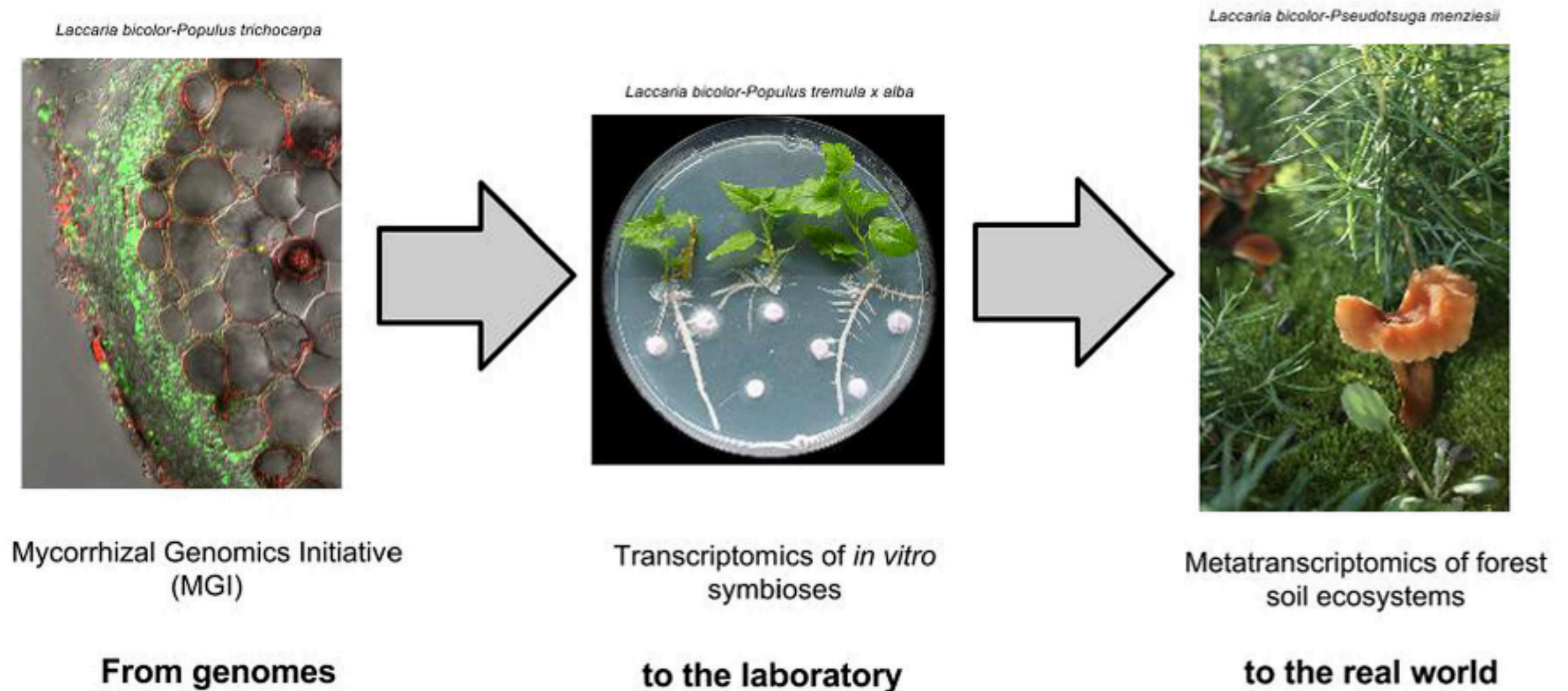


FIGURE 1 | From sequence to function of symbiotic genes. Understanding evolution and function of mycorrhizal interactions can be driven by large scale genomics, transcriptomics and metatranscriptomics studies.

“The biochemical, genetic and transcriptos experiments are being aided by massive effort to sequence the genomes of multiple mycorrhizal fungi.”

The first three of those genomes to be published:

- ▶ ECM basidiomycete *Laccaria bicolor*
- ▶ ECM ascomycete *Tuber melanosporum*
- ▶ AM glomeromycete *Rhizophagus irregularis*

L. bicolor

Led directly to identification of many categories of molecules potentially involved in symbiosis:

Secreted proteases, lipases, carbohydrate-active enzymes (CAZymes), enzymes for all core carbohydrate metabolic pathways, and for fatty acid metabolism, transporters of hexoses and of nitrogenous compounds, multicopper oxidases, antioxidant enzymes, signal transduction protein kinases and small GTPases, hydrophobins, mating type loci.

Molecular manipulation of the organism complements genomics

RNA silencing methodology has been developed to knockdown genes in *L. bicolor*



Such experiments have demonstrated that nitrate reductase and nitrate transporter and a mycorrhiza-induced small secreted protein are involved in symbiosis.

Un genoma secuenciado permite la aplicación de estudios “top-down” sobre los potenciales symbiosis genes.

Comparación con otros genomas de Agaricales



Genoma grande, atribuido a a TEs y un gran número de familias de genes

El genoma carece de invertasas, así como de muchas familias de enzimas degradadoras de la pared celular (PCWDE)



***L. bicolor* depende de su planta hospedera para los carbohidratos y no activa las defensas del hospedero**

Transcriptomics enlaces genome analysis by showing expresion and regulación

Large set of small secreted proteins (SSPs)



**Transcriptomics showed that some of SSPs are differentially exprese between
free-living mycelia and mycorrhizae**

These MiSSPs appear specific to *L. bicolor*

7- kD MiSSP7

The most highly inducible of these genes

MiSSP7 interacts with poplar protein PtJAZ6 a negative regulator of jasmonic acid (JA)-induced gene regulation in poplar

Blocks or mitigates the impact of JA on *L. bicolor* colonization of host roots.

The mycorrhizal lifestyle can evolve through loss of PCWDEs and expansion of lineage-specific gene families, such as SSP effectors.

Tuber melanosporum

The sequenced genome facilitated the identification and analysis of many gene families of interest to symbiosis studies



CAZymes

Lipases

Multicopper oxidases

An invertase

Other carbohydrate metabolism enzymes

Metal detoxification genes

Cell wall metabolism enzymes

ECM tope can evolve without expansion of families and thus a different set of symbiosis genes

The AM *Rhizophagus irregularis*

The genome allowed cloning and characterization of monosaccharide transporters both specific to and required for the symbiosis

Some signal transduction pathway genes

The CAZyme repertoire was more reduced than *L. bicolor*

Transcriptomics revealed a modest set of symbiosis-upregulated genes

Despite enormous phylogenetic distance and morphological difference symbiosis can involve similar solutions as symbiosis-induced SSPs and loss of PCWDEs

Table 1 | Properties of the first sequenced mycorrhizal fungal genomes.

Species	<i>Laccaria bicolor</i>	<i>Tuber melanosporum</i>	<i>Rhizophagus irregularis</i>
Phylogeny	Basidiomycota, Agaricales	Ascomycota, Pezizales	Glomeromycota, Glomerales
Mycorrhizal morphotype	Ectomycorrhiza	Ectomycorrhiza	Arbuscular mycorrhiza
Plant partners	Broad range of forest trees, hardwoods and conifers, such as poplars and firs	Narrow range of forest trees, hardwoods and conifers, such as hazel tree and oaks	Hundreds of herbaceous plant species, including crops such as wheat and rice
Genomic assembly (Mbp)	60.7	125.0	91.1
Repeat-masked total (Mbp)	15.1 (25%)	65.3 (52%)	14.0 (15%)
# Predicted genes	23132	7496	30282
Average # exons/gene	5.28	3.87	3.46
# Predicted gene families	3523	199	2149
Average # genes/family	5.02	3.79	8.00
Average protein length (aa)	356	439	270
# Predicted signal peptides	3201 (14%)	1224 (16%)	1995 (7%)
# Distinct Pfam domains	2348	2272	2469
Major publication	Martin et al. (2008)	Martin et al. (2010)	Tisserant et al. (2013)

All numbers are calculated from the genomes' computationally reconstructed assemblies and annotations.

Conclusiones

The three genomes provide a solid base for addressing fundamental questions about nature and role of vital mutualism

They revealed potential molecular mechanism underpinning these symbiosis and offered a first glimpse of evolution of different type of mycorrhizae.

Comparative genomics did not reveal any universal “symbiosis genes” but did demonstrate convergent of genomic features

Thus, while the mycorrhizal symbiosis now appears unlikely to be defined by a set of universal “symbiosis genes” it may be explained by convergent traits that independently and repeatedly evolved